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<110> Jegla, Timothy James
ICAgen, Inc.

<120> KCNQ5, a Novel Potassium Channel

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<140> US 09/810,796

<141> 2001-03-15

<150> US 60/190,954

<151> 2000-03-21

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<170> PatentIn Ver. 2.1

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potassium channel KCNQ5-1

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potassium channel KCNQ5-1 coding sequence

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<222> (1)..(2694)

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Gly Ala Arg Met Ser Leu Leu Gly Lys Pro Leu Ser Tyr Thr Ser Ser
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Gln Ser Cys Arg Arg Asn Val Lys Tyr Arg Arg Val Gln Asn Tyr Leu
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Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His Ala
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 Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val
 210 215 220
 Tyr Ala His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu
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 Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Thr Pro Leu Thr Trp Leu
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 Pro Pro Leu Lys Thr Val Ile Arg Ala Ile Arg Ile Met Lys Phe His
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 Asp Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Cys Arg
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 770 775 780
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 potassium channel KCNQ5-2

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 Gly Ala Arg Met Ser Leu Leu Gly Lys Pro Leu Ser Tyr Thr Ser Ser
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 Gln Ser Cys Arg Arg Asn Val Lys Tyr Arg Arg Val Gln Asn Tyr Leu
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Val Ser Ile Ala Thr Trp Lys Pro His Leu Lys Ala Leu His Thr Cys
355 360 365
Ser Pro Thr Asn Gln Lys Leu Ser Phe Lys Glu Arg Val Arg Met Ala
370 375 380
Ser Pro Arg Gly Gln Ser Ile Lys Ser Arg Gln Ala Ser Val Gly Asp
385 390 395 400
Arg Arg Ser Pro Ser Thr Asp Ile Thr Ala Glu Gly Ser Pro Thr Lys
405 410 415
Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Pro Ser
420 425 430
Leu Arg Leu Lys Ser Ser Gln Pro Lys Pro Val Ile Asp Ala Asp Thr
435 440 445
Ala Leu Gly Thr Asp Asp Val Tyr Asp Glu Lys Gly Cys Gln Cys Asp
450 455 460
Val Ser Val Glu Asp Leu Thr Pro Pro Leu Lys Thr Val Ile Arg Ala
465 470 475 480
Ile Arg Ile Met Lys Phe His Val Ala Lys Arg Lys Phe Lys Glu Thr
485 490 495
Leu Arg Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr Ser Ala Gly
500 505 510
His Leu Asp Met Leu Cys Arg Ile Lys Ser Leu Gln Thr Arg Val Asp
515 520 525
Gln Ile Leu Gly Lys Gly Gln Ile Thr Ser Asp Lys Lys Ser Arg Glu
530 535 540
Lys Ile Thr Ala Glu His Glu Thr Thr Asp Asp Leu Ser Met Leu Gly
545 550 555 560
Arg Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu Ser Lys Leu
565 570 575

Asp Cys Leu Leu Asp Ile Tyr Gln Gln Val Leu Arg Lys Gly Ser Ala
 580 585 590
 Ser Ala Leu Ala Leu Ala Ser Phe Gln Ile Pro Pro Phe Glu Cys Glu
 595 600 605
 Gln Thr Ser Asp Tyr Gln Ser Pro Val Asp Ser Lys Asp Leu Ser Gly
 610 615 620
 Ser Ala Gln Asn Ser Gly Cys Leu Ser Arg Ser Thr Ser Ala Asn Ile
 625 630 635 640
 Ser Arg Gly Leu Gln Phe Ile Leu Thr Pro Asn Glu Phe Ser Ala Gln
 645 650 655
 Thr Phe Tyr Ala Leu Ser Pro Thr Met His Ser Gln Ala Thr Gln Val
 660 665 670
 Pro Ile Ser Gln Ser Asp Gly Ser Ala Val Ala Ala Thr Asn Thr Ile
 675 680 685
 Ala Asn Gln Ile Asn Thr Ala Pro Lys Pro Ala Ala Pro Thr Thr Leu
 690 695 700
 Gln Ile Pro Pro Pro Leu Pro Ala Ile Lys His Leu Pro Arg Pro Glu
 705 710 715 720
 Thr Leu His Pro Asn Pro Ala Gly Leu Gln Glu Ser Ile Ser Asp Val
 725 730 735
 Thr Thr Cys Leu Val Ala Ser Lys Glu Asn Val Gln Val Ala Gln Ser
 740 745 750
 Asn Leu Thr Lys Asp Arg Ser Met Arg Lys Ser Phe Asp Met Gly Gly
 755 760 765
 Glu Thr Leu Leu Ser Val Cys Pro Met Val Pro Lys Asp Leu Gly Lys
 770 775 780
 Ser Leu Ser Val Gln Asn Leu Ile Arg Ser Thr Glu Glu Leu Asn Ile
 785 790 795 800
 Gln Leu Ser Gly Ser Glu Ser Ser Gly Ser Arg Gly Ser Gln Asp Phe
 805 810 815
 Tyr Pro Lys Trp Arg Glu Ser Lys Leu Phe Ile Thr Asp Glu Glu Val
 820 825 830
 Gly Pro Glu Glu Thr Glu Thr Asp Thr Phe Asp Ala Ala Pro Gln Pro
 835 840 845
 Ala Arg Glu Ala Ala Phe Ala Ser Asp Ser Leu Arg Thr Gly Arg Ser
 850 855 860
 Arg Ser Ser Gln Ser Ile Cys Lys Ala Gly Glu Ser Thr Asp Ala Leu
 865 870 875 880
 Ser Leu Pro His Val Lys Leu Lys
 885

<210> 6
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense primer
 (1)

<400> 6
 ccacgtctgc actcaggaag tctccg

26

<210> 7
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense
primer (2)

<400> 7
ccagcttgga ttctatggac tgtacc

26

<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:standard 3'
RACE PCR gene specific primer (3)

<400> 8
gaagagccga gagaaaataa cagcag

26

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:reamplification
gene-specific oligo (4)

<400> 9
gccctgtgga tagcaaagat ctttcg

26

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested standard
5' RACE PCR gene specific oligo (5)

<400> 10
gctgtgagca taaaccactg aaccc

25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested standard
5' RACE PCR gene specific oligo (6)

<400> 11
ccatgcgcac catgcggagg atctg

25

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amplification
 primer

<400> 12
 catgaaggat gtggagtcgg g

21

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amplification
 primer

<400> 13
 tggctaaaga actgctatgc ctgg

24

<210> 14
 <211> 844
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human KCNQ2

<400> 14
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 Glu Lys Lys Leu Lys Val Gly Phe Val Gly Leu Asp Pro Gly Ala Pro
 20 25 30
 Asp Ser Thr Arg Asp Gly Ala Leu Leu Ile Ala Gly Ser Glu Ala Pro
 35 40 45
 Lys Arg Gly Ser Ile Leu Ser Lys Pro Arg Ala Gly Gly Ala Gly Ala
 50 55 60
 Gly Lys Pro Pro Lys Arg Asn Ala Phe Tyr Arg Lys Leu Gln Asn Phe
 65 70 75 80
 Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile Tyr His
 85 90 95
 Ala Tyr Val Phe Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Phe
 100 105 110
 Ser Thr Ile Lys Glu Tyr Glu Lys Ser Ser Glu Gly Ala Leu Tyr Ile
 115 120 125
 Leu Glu Ile Val Thr Ile Val Val Phe Gly Val Glu Tyr Phe Val Arg
 130 135 140
 Ile Trp Ala Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Arg Gly Arg
 145 150 155 160
 Leu Lys Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Ile Met Val Leu
 165 170 175
 Ile Ala Ser Ile Ala Val Leu Ala Ala Gly Ser Gln Gly Asn Val Phe
 180 185 190
 Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu Arg Met
 195 200 205

Ile Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val
 210 215 220
 Val Tyr Ala His Ser Lys Glu Leu Val Thr Ala Trp Tyr Ile Gly Phe
 225 230 235 240
 Leu Cys Leu Ile Leu Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Gly
 245 250 255
 Glu Asn Asp His Phe Asp Thr Tyr Ala Asp Ala Leu Trp Trp Gly Leu
 260 265 270
 Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Tyr Pro Gln Thr Trp
 275 280 285
 Asn Gly Arg Leu Leu Ala Ala Thr Phe Thr Leu Ile Gly Val Ser Phe
 290 295 300
 Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val
 305 310 315 320
 Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn Pro Ala
 325 330 335
 Ala Gly Leu Ile Gln Ser Ala Trp Arg Phe Tyr Ala Thr Asn Leu Ser
 340 345 350
 Arg Thr Asp Leu His Ser Thr Trp Gln Tyr Tyr Glu Arg Thr Val Thr
 355 360 365
 Val Pro Met Tyr Arg Leu Ile Pro Pro Leu Asn Gln Leu Glu Leu Leu
 370 375 380
 Arg Asn Leu Lys Ser Lys Ser Gly Leu Ala Phe Arg Lys Asp Pro Pro
 385 390 395 400
 Pro Glu Pro Ser Pro Ser Gln Lys Val Ser Leu Lys Asp Arg Val Phe
 405 410 415
 Ser Ser Pro Arg Gly Val Ala Ala Lys Gly Lys Gly Ser Pro Gln Ala
 420 425 430
 Gln Thr Val Arg Arg Ser Pro Ser Ala Asp Gln Ser Leu Glu Asp Ser
 435 440 445
 Pro Ser Lys Val Pro Lys Ser Trp Ser Phe Gly Asp Arg Ser Arg Ala
 450 455 460
 Arg Gln Ala Phe Arg Ile Lys Gly Ala Ala Ser Arg Gln Asn Ser Glu
 465 470 475 480
 Glu Ala Ser Leu Pro Gly Glu Asp Ile Val Asp Asp Lys Ser Cys Pro
 485 490 495
 Cys Glu Phe Val Thr Glu Asp Leu Thr Pro Gly Leu Lys Val Ser Ile
 500 505 510
 Arg Ala Val Cys Val Met Arg Phe Leu Val Ser Lys Arg Lys Phe Lys
 515 520 525
 Glu Ser Leu Arg Pro Tyr Asp Val Met Asp Val Ile Glu Gln Tyr Ser
 530 535 540
 Ala Gly His Leu Asp Met Leu Ser Arg Ile Lys Ser Leu Gln Ser Arg
 545 550 555 560
 Val Asp Gln Ile Val Gly Arg Gly Pro Ala Ile Thr Asp Lys Asp Arg
 565 570 575
 Thr Lys Gly Pro Ala Glu Ala Glu Leu Pro Glu Asp Pro Ser Met Met
 580 585 590
 Gly Arg Leu Gly Lys Val Glu Lys Gln Val Leu Ser Met Glu Lys Lys
 595 600 605
 Leu Asp Phe Leu Val Asn Ile Tyr Met Gln Arg Met Gly Ile Pro Pro
 610 615 620
 Thr Glu Thr Glu Ala Tyr Phe Gly Ala Lys Glu Pro Glu Pro Ala Pro
 625 630 635 640
 Pro Tyr His Ser Pro Glu Asp Ser Arg Glu His Val Asp Arg His Gly
 645 650 655
 Cys Ile Val Lys Ile Val Arg Ser Ser Ser Ser Thr Gly Gln Lys Asn
 660 665 670
 Phe Ser Ala Pro Pro Ala Ala Pro Pro Val Gln Cys Pro Pro Ser Thr
 675 680 685

Ser	Trp	Gln	Pro	Gln	Ser	His	Pro	Arg	Gln	Gly	His	Gly	Thr	Ser	Pro
690						695					700				
Val	Gly	Asp	His	Gly	Ser	Leu	Val	Arg	Ile	Pro	Pro	Pro	Pro	Ala	His
705						710				715					720
Glu	Arg	Ser	Leu	Ser	Ala	Tyr	Gly	Gly	Gly	Asn	Arg	Ala	Ser	Met	Glu
					725					730					735
Phe	Leu	Arg	Gln	Glu	Asp	Thr	Pro	Gly	Cys	Arg	Pro	Pro	Glu	Gly	Thr
					740			745					750		
Leu	Arg	Asp	Ser	Asp	Thr	Ser	Ile	Ser	Ile	Pro	Ser	Val	Asp	His	Glu
		755					760					765			
Glu	Leu	Glu	Arg	Ser	Phe	Ser	Gly	Phe	Ser	Ile	Ser	Gln	Ser	Lys	Glu
	770					775					780				
Asn	Leu	Asp	Ala	Leu	Asn	Ser	Cys	Tyr	Ala	Ala	Val	Ala	Pro	Cys	Ala
785						790				795					800
Lys	Val	Arg	Pro	Tyr	Ile	Ala	Glu	Gly	Glu	Ser	Asp	Thr	Asp	Ser	Asp
				805					810						815
Leu	Cys	Thr	Pro	Cys	Gly	Pro	Pro	Pro	Arg	Ser	Ala	Thr	Gly	Glu	Gly
			820					825					830		
Pro	Phe	Gly	Asp	Val	Gly	Trp	Ala	Gly	Pro	Arg	Lys				
		835					840								

<210> 15
 <211> 695
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human KCNQ4

<400> 15

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			20					25					30		
Gln	Gly	Glu	Ala	Gly	Gly	Gly	Gly	Ser	Pro	Arg	Arg	Leu	Gly	Leu	Leu
		35					40					45			
Gly	Ser	Pro	Leu	Pro	Pro	Gly	Ala	Pro	Leu	Pro	Gly	Pro	Gly	Ser	Gly
	50					55					60				
Ser	Gly	Ser	Ala	Cys	Gly	Gln	Arg	Ser	Ser	Ala	Ala	His	Lys	Arg	Tyr
65					70					75					80
Arg	Arg	Leu	Gln	Asn	Trp	Val	Tyr	Asn	Val	Leu	Glu	Arg	Pro	Arg	Gly
				85					90					95	
Trp	Ala	Phe	Val	Tyr	His	Val	Phe	Ile	Phe	Leu	Leu	Val	Phe	Ser	Cys
			100				105						110		
Leu	Val	Leu	Ser	Val	Leu	Ser	Thr	Ile	Gln	Glu	His	Gln	Glu	Leu	Ala
		115					120					125			
Asn	Glu	Cys	Leu	Leu	Ile	Leu	Glu	Phe	Val	Met	Ile	Val	Val	Phe	Gly
	130					135				140					
Leu	Glu	Tyr	Ile	Val	Arg	Val	Trp	Ser	Ala	Gly	Cys	Cys	Cys	Arg	Tyr
145					150					155					160
Arg	Gly	Trp	Gln	Gly	Arg	Phe	Arg	Phe	Ala	Arg	Lys	Pro	Phe	Cys	Val
			165						170					175	
Ile	Asp	Phe	Ile	Val	Phe	Val	Ala	Ser	Val	Ala	Val	Ile	Ala	Ala	Gly
			180				185						190		
Thr	Gln	Gly	Asn	Ile	Phe	Ala	Thr	Ser	Ala	Leu	Arg	Ser	Met	Arg	Phe
	195						200					205			
Leu	Gln	Ile	Leu	Arg	Met	Val	Arg	Met	Asp	Arg	Arg	Gly	Gly	Thr	Trp
	210					215					220				
Lys	Leu	Leu	Gly	Ser	Val	Val	Tyr	Ala	His	Ser	Lys	Glu	Leu	Ile	Thr
225					230					235					240

Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
 245 250 255
 Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
 260 265 270
 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
 275 280 285
 Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala
 290 295 300
 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
 305 310 315 320
 Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu
 325 330 335
 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu
 340 345 350
 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
 355 360 365
 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
 370 375 380
 His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg
 385 390 395 400
 Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala
 405 410 415
 Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser
 420 425 430
 Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg
 435 440 445
 Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser
 450 455 460
 Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln
 465 470 475 480
 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
 485 490 495
 Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala
 500 505 510
 Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro
 515 520 525
 Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val
 530 535 540
 Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
 545 550 555 560
 Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
 565 570 575
 Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
 580 585 590
 Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu
 595 600 605
 Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
 610 615 620
 Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
 625 630 635 640
 Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
 645 650 655
 Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val
 660 665 670
 Asp His Glu Asp Ile Ser Val Ser Ala Gln Thr Leu Ser Ile Ser Arg
 675 680 685
 Ser Val Ser Thr Asn Met Asp
 690 695

<210> 16
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sense
oligonucleotide (7)

<400> 16
ctctgaattc caccatgaag gatgtggagt cggg

34

<210> 17
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:antisense
oligonucleotide (8)

<400> 17
aatgtctaga atggctaaag aactgctatg cctgg

35